

## SEQUENCE LISTING

<110> MASTERNAK, Krzysztof  
 REITH, Walter  
 MACH, Bernard

<120> New Transcription Factors of Class II Genes, Substances  
 Capable of Inhibiting This New Transcription Factor and  
 Medical Uses of These Substances

<130> 010830-117

<140> US 09/840,243

<141> 2001-04-24

<150> EP 98120085.0

<151> 1998-10-24

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 1

ccgtacgcgt ctagaccatg gagcttaccc agcctgcaga

40

<210> 2

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 2

ttcgaattct cgagtgtctg agtccccggc a

31

<210> 3

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 3

ccgtacgcgt ctagaccatg gagcccactc aggttgc

37

<210> 4

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 4

ttcgaattct cgagtgctg ggttccagca gg

32

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 5

ccagctctag actccaccac tctcaccaac

30

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 6

ccttcgaatt ctcgctcttt tgccaggatg

30

<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;400&gt; 7

ggttctctag attggcagca ctggggatag

30

&lt;210&gt; 8

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;400&gt; 8

gctacgaatt ccagcagaca cagccaaaac

30

&lt;210&gt; 9

&lt;211&gt; 69

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;400&gt; 9

ccgtacgcgt ctagaatgga ttacaaagac gatgacgata agatggagct taccagcct 60

gcagaagac

69

&lt;210&gt; 10

&lt;211&gt; 1345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (418) .. (1200)

&lt;400&gt; 10

acgcaggga ggaggcacac ccgggggtgg cgcagtgagg agggggcgcg acggccagga 60

ggctggtgga gcgacacca ggcaggagag ggggaagaac tctctcctt tctgaacccc 120

cttttccttg agagacgagt tgggggagtc ctccacgcat taccactcg ggccgcaaaa 180

actcccttct ttagccctct gccccgccc ttgcttataa gcctttgaga ccgcagaagg 240

gaccttggtg tggaacggga cggccaagag gaagccagat cgctgagggt ccggtctcca 300  
 gtttgccctcc tgctatatcc attggaagag aaaagtttgt gacttggggcc cccaagtttt 360  
 gagagaactg ggcttttcggc gcgggggggac agaggaggct cgtgggggagc tttcccc 417  
 atg gag ctt acc cag cct gca gaa gac ctc atc cag acc cag cag acc 465  
 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr  
 1 5 10 15  
 cct gcc tca gaa ctt ggg gac cct gaa gac ccc gga gag gag gct gca 513  
 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala  
 20 25 30  
 gat ggc tca gac act gtg gtc ctc agt ctc ttt ccc tgc acc cct gag 561  
 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu  
 35 40 45  
 cct gtg aat cct gaa ccg gat gcc agt gtt tcc tct cca cag gca ggc 609  
 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly  
 50 55 60  
 agc tcc ctg aag cac tcc acc act ctc acc aac cgg cag cga ggg aac 657  
 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn  
 65 70 75 80  
 gag gtg tca gct ctg ccg gcc acc cta gac tcc ctg tcc atc cac cag 705  
 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln  
 85 90 95  
 ctc gca gca cag ggg gag ctg gac cag ctg aag gag cat ttg cgg aaa 753  
 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys  
 100 105 110  
 ggt gac aac ctc gtc aac aag cca gac gag cgc ggc ttc acc ccc ctc 801  
 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu  
 115 120 125  
 atc tgg gcc tcc gcc ttt gga gag att gag acc gtt cgc ttc ctg ctg 849  
 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu  
 130 135 140  
 gag tgg ggt gcc gac ccc cac atc ctg gca aaa gag cga gag agc gcc 897  
 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala  
 145 150 155 160  
 ctg tcg ctg gcc agc aca ggc ggc tac aca gac att gtg ggg ctg ctg 945  
 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu  
 165 170 175

ctg gag cgt gac gtg gac atc aac atc tat gat tgg aat gga ggg acg 993  
 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr  
                   180                                  185                                  190

cca ctg ctg tac gct gtg cgc ggg aac cac gtg aaa tgc gtt gag gcc 1041  
 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala  
                   195                                  200                                  205

ttg ctg gcc cga ggc gct gac ctc acc acc gaa gcc gac tct ggc tac 1089  
 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr  
                   210                                  215                                  220

acc ccg atg gac ctt gcc gtg gcc ctg gga tac cgg aaa gtg caa cag 1137  
 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln  
                   225                                  230                                  235                                  240

gtg atc gag aac cac atc ctc aag ctc ttc cag agc aac ctg gtg ccc 1185  
 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro  
                                   245                                  250                                  255

gct gac cct gag tga aggccgcctg ccggggactc agacactcag ggaacaaaat 1240  
 Ala Asp Pro Glu  
                   260

ggtcagccag agctggggaa acccagaact gacttcaaag gcagcttctg gacaggtggt 1300

gggaggggac ccttcccaag aggaaccaat aaaccttctg tgcag 1345

<210> 11  
 <211> 260  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr  
   1                                  5                                  10                                  15  
 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala  
                   20                                  25                                  30  
 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu  
                   35                                  40                                  45  
 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly  
                   50                                  55                                  60  
 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn  
   65                                  70                                  75                                  80

Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln  
                     85                    90                    95  
 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys  
                     100                    105                    110  
 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu  
                     115                    120                    125  
 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu  
                     130                    135                    140  
 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala  
                     145                    150                    155                    160  
 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu  
                     165                    170                    175  
 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr  
                     180                    185                    190  
 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala  
                     195                    200                    205  
 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr  
                     210                    215                    220  
 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln  
                     225                    230                    235                    240  
 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro  
                     245                    250                    255  
 Ala Asp Pro Glu  
                     260

&lt;210&gt; 12

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr

1	5	10	15
Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala	20	25	30
Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu	35	40	45
Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly	50	55	60
Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn	65	70	75
Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln	85	90	95
Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys	100	105	110
Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu	115	120	125
Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu	130	135	140
Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala	145	150	155
Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu	165	170	175
Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr	180	185	190
Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala	195	200	205
Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr	210	215	220
Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln	225	230	235
Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro	245	250	255
Ala Asp Pro Glu	260		

<210> 13  
 <211> 269  
 <212> PRT  
 <213> Murinae gen. sp.

<400> 13  
 Met Glu Pro Thr Gln Val Ala Glu Asn Leu Val Pro Asn Gln Gln Pro  
   1                  5                  10                  15  
 Pro Val Pro Asp Leu Glu Asp Pro Glu Asp Thr Arg Asp Glu Ser Pro  
                   20                  25                  30  
 Glu Asn Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Asp  
                   35                  40                  45  
 Ala Val Asn Pro Glu Ala Asp Ala Ser Ala Ser Ser Leu Gln Gly Ser  
                   50                  55                  60  
 Phe Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn Glu  
   65                  70                  75                  80  
 Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln Leu  
                   85                  90                  95  
 Ala Ala Gln Gly Glu Leu Ser Gln Leu Lys Asp His Leu Arg Lys Gly  
                   100                  105                  110  
 Ala Cys Pro Ala Cys Thr Cys Leu Ser Gly Asn Asn Leu Ile Asn Lys  
                   115                  120                  125  
 Pro Asp Glu Arg Gly Phe Thr Pro Leu Ile Trp Ala Ser Ala Phe Gly  
                   130                  135                  140  
 Glu Ile Glu Thr Val Arg Phe Leu Leu Asp Trp Gly Ala Asp Pro His  
   145                  150                  155                  160  
 Ile Leu Ala Lys Glu Arg Glu Ser Ala Leu Ser Leu Ala Ser Met Gly  
                   165                  170                  175  
 Gly Tyr Thr Asp Ile Val Arg Leu Leu Leu Asp Arg Asp Val Asp Ile  
                   180                  185                  190  
 Asn Ile Tyr Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val Arg  
                   195                  200                  205  
 Gly Asn His Val Lys Cys Val Glu Ala Leu Leu Ala Arg Gly Ala Asp  
                   210                  215                  220  
 Leu Thr Thr Glu Ala Asp Ser Gly Tyr Thr Pro Met Asp Leu Ala Val  
   225                  230                  235                  240



Ala Leu Gly Tyr Arg Lys Val Gln Gln Val Met Glu Ser His Ile Leu  
 245 250 255

Arg Leu Phe Gln Ser Thr Leu Gly Pro Val Asp Pro Glu  
 260 265

<210> 14  
 <211> 111  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(111)

<400> 14  
 acc cta gac tgg tgc cga ccc cca cat cct ggc aaa aga gcg aga gag 48  
 Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu  
 1 5 10 15

cgc cct gtc gct ggc cag cac agg cgg cta cac aga cat tgt ggg gct 96  
 Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala  
 20 25 30

gct gct gga gcg tga 111  
 Ala Ala Gly Ala  
 35

<210> 15  
 <211> 36  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu  
 1 5 10 15

Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala  
 20 25 30

Ala Ala Gly Ala  
 35

<210> 16  
 <211> 42  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (31)..(42)

&lt;400&gt; 16

ctggtggtat tgcccgctc ctctgccag gtg aca acc tcg

42

&lt;210&gt; 17

&lt;211&gt; 74

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(27)

&lt;400&gt; 17

gag acc gtt cgc ttc ctg ctg gag tgg gtgcgtccca gccagctgg

47

gcagctgggg ggttcccggg ggcctta

74

&lt;210&gt; 18

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (31)..(159)

<223> Amino acids at positions 31, 148 and 159 are Xaa wherein  
Xaa = any amino acid.

&lt;400&gt; 18

Asn	Ala	Phe	Asn	Val	Phe	Thr	Phe	Val	Phe	His	Leu	Ala	Glu	Cys	Asn
1				5				10						15	

Ile	His	Thr	Ser	Pro	Ser	Pro	Gly	Ile	Gln	Val	Arg	His	Val	Xaa	Thr
			20					25						30	

Pro	Ser	Thr	Thr	Lys	His	Phe	Ser	Pro	Ile	Lys	Gln	Ser	Thr	Thr	Leu
			35				40					45			

Thr	Asn	Lys	His	Arg	Gly	Asn	Glu	Val	Ser	Thr	Thr	Pro	Leu	Leu	Ala
	50					55						60			

Asn	Ser	Leu	Ser	Val	His	Gln	Leu	Ala	Ala	Gln	Gly	Glu	Met	Leu	Tyr
65					70					75				80	

Leu Ala Thr Arg Ile Glu Gln Glu Asn Val Ile Asn His Thr Asp Glu  
85 90 95

Glu Gly Phe Thr Pro Leu Met Trp Ala Ala Ala His Gly Gln Ile Ala  
100 105 110

Val Val Glu Phe Leu Leu Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly  
115 120 125

Lys Gly Arg Glu Ser Ala Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr  
130 135 140

Asp Ile Val Xaa Met Leu Leu Asp Cys Gly Val Asp Val Asn Xaa Tyr  
145 150 155 160

Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val His Gly Asn His  
165 170 175

Val Lys Cys Val Lys Met Leu Leu Glu Ser Gly Ala Asp Pro Thr Ile  
180 185 190

Glu Thr Asp Ser Gly Tyr Asn Ser Met Asp Leu Ala Val Ala Leu Gly  
195 200 205

Ile Glu Val Phe Asn Arg Leu Leu Ser His Ile Cys  
210 215 220

<210> 19

<211> 218

<212> PRT

<213> Murinae gen. sp.

<400> 19

Ala Ser Val Leu Phe Lys Ala Glu Cys Asn Ile His Thr Ser Pro Ser  
1 5 10 15

Pro Gly Ile Gln Val Arg His Val Tyr Thr Pro Ser Thr Thr Lys His  
20 25 30

Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu Thr Asn Lys His Arg Gly  
35 40 45

Asn Glu Val Ser Thr Thr Pro Leu Leu Ala Asn Ser Leu Ser Ala His  
50 55 60

Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr Leu Ala Thr Arg Ile Glu  
65 70 75 80

Gln Glu Asn Val Ile Asn His Thr Asp Glu Glu Gly Phe Thr Pro Leu

85

90

95

Met Trp Ala Ala Ala His Gly Gln Ile Ala Val Val Glu Phe Leu Leu  
                   100                                  105                                  110

Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly Lys Gly Arg Glu Ser Ala  
                   115                                  120                                  125

Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr Asp Ile Val Lys Met Leu  
                   130                                  135                                  140

Leu Asp Cys Gly Val Asp Val Asn Glu Tyr Asp Trp Asn Gly Gly Thr  
                   145                                  150                                  155                                  160

Pro Leu Leu Tyr Ala Gly His Gly Asn His Val Lys Cys Val Lys Met  
                   165                                  170                                  175

Leu Leu Glu Asn Gly Ala Asp Pro Thr Ile Glu Thr Asp Ser Gly Tyr  
                   180                                  185                                  190

Asn Ser Met Asp Leu Ala Val Ala Leu Gly Ile Glu Gly Cys Ser Asp  
                   195                                  200                                  205

Tyr Met Leu Val Thr Asp Val Phe Arg Ile  
                   210                                  215

&lt;210&gt; 20

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:FLAG epitope

&lt;400&gt; 20

Asp Tyr Lys Asp Asp Asp Asp Lys  
   1                                  5

&lt;210&gt; 21

&lt;211&gt; 14

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:DRA promoter template

&lt;400&gt; 21

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ggaccctttg caag

<210> 22  
<211> 14  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DRA promoter template

<400> 22  
tacatagcgt acgt

14